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## Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a sample screen of LALNVIEW and access its documentation.

### Results of SIM with:

Sequence 1: UserSeq3, (205 residues)

protein encoded by SEQ ID NO:3

Sequence 2: UserSeq1, (205 residues)

SEQ ID NO:1

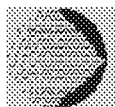
### using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

100.0% identity in 205 residues overlap; Score: 1078.0; Gap frequency: 0.0%

```
UserSeq3,      1 MTENILRKSDEEIQKEITARVKALESM LIEQGILTTSMIDRMAE IYENEVGPHLGAKVVV
UserSeq1,      1 MTENILRKSDEEIQKEITARVKALESM LIEQGILTTSMIDRMAE IYENEVGPHLGAKVVV
                *****

UserSeq3,     61 KAWTDPEFKKRLLADGTEACKELGIGGLQGEDMMWVENTDEVHHVVVCTLCSCYPWPVLG
UserSeq1,     61 KAWTDPEFKKRLLADGTEACKELGIGGLQGEDMMWVENTDEVHHVVVCTLCSCYPWPVLG
                *****

UserSeq3,    121 LPPNWFKEPQYRSRVVREPRQLLKEEF GF EVPPSKEIKVWDS SSEMRFVVL PQRPA GTDG
UserSeq1,    121 LPPNWFKEPQYRSRVVREPRQLLKEEF GF EVPPSKEIKVWDS SSEMRFVVL PQRPA GTDG
                *****

UserSeq3,    181 WSEEE LATLV TRESMIGVEPAKAVA
UserSeq1,    181 WSEEE LATLV TRESMIGVEPAKAVA
                *****
```

---

22.2% identity in 18 residues overlap; Score: 31.0; Gap frequency: 0.0%

UserSeq3,        65 DPEFKKRLLDGTEACK  
UserSeq1,       128 EPQYRSRVVREPRQLLKE  
                 \*       \*       \*\*

---

22.2% identity in 18 residues overlap; Score: 31.0; Gap frequency: 0.0%

UserSeq3,       128 EPQYRSRVVREPRQLLKE  
UserSeq1,        65 DPEFKKRLLDGTEACK  
                 \*       \*       \*\*

---

20.0% identity in 20 residues overlap; Score: 23.0; Gap frequency: 0.0%

UserSeq3,        44 EIYENEVGPLGAKVVVKAW  
UserSeq1,       141 QLLKEEFGFEVPPSKEIKVW  
                 \* \*       \* \*

---

20.0% identity in 20 residues overlap; Score: 23.0; Gap frequency: 0.0%

UserSeq3,       141 QLLKEEFGFEVPPSKEIKVW  
UserSeq1,        44 EIYENEVGPLGAKVVVKAW  
                 \* \*       \* \*

---

36.4% identity in 11 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq3,        64 TDPEFKKRLLA  
UserSeq1,        9 SDEEIQKEITA  
                 \* \* \* \*

---

36.4% identity in 11 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq3,        9 SDEEIQKEITA  
UserSeq1,       64 TDPEFKKRLLA  
                 \* \* \* \*

---

40.0% identity in 10 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq3,       182 SEEELATLVT  
UserSeq1,        9 SDEEIQKEIT  
                 \* \*\* \*

---

40.0% identity in 10 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq3,        9 SDEEIQKEIT  
UserSeq1,       182 SEEELATLVT

\* \*\* \*

---

31.2% identity in 16 residues overlap; Score: 20.0; Gap frequency: 0.0%

UserSeq3, 142 LLKEEFGFEVPPSKEI  
UserSeq1, 189 LVTRESMIGVEPAKAV  
\* \* \* \* \*

---

31.2% identity in 16 residues overlap; Score: 20.0; Gap frequency: 0.0%

UserSeq3, 189 LVTRESMIGVEPAKAV  
UserSeq1, 142 LLKEEFGFEVPPSKEI  
\* \* \* \* \*

---

19.0% identity in 21 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 1 MTENILRKSDEEIQKEITARV  
UserSeq1, 38 MIDRMAEIIYENEVGPLGAKV  
\* \* \* \*

---

40.0% identity in 5 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 181 WSEEE  
UserSeq1, 63 WTDPE  
\* \*

---

35.3% identity in 17 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 143 LKEEFGFEVPPSKEIKV  
UserSeq1, 42 MAEIIYENEVGPLGAKV  
\* \*\* \* \*\*

---

40.0% identity in 5 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 63 WTDPE  
UserSeq1, 181 WSEEE  
\* \*

---

17.6% identity in 17 residues overlap; Score: 18.0; Gap frequency: 0.0%

UserSeq3, 1 MTENILRKSDEEIQKEI  
UserSeq1, 34 LTTSMIDRMAEIIYENEV  
\* \* \*

---

17.6% identity in 17 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,      34 LTTSMIDRMAEIIYENEV
UserSeq1,       1 MTENILRKSDEEIQKEI
                *      *      *
```

---

19.0% identity in 21 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,      38 MIDRMAEIIYENEVGPHLGAKV
UserSeq1,       1 MTENILRKSDEEIQKEITARV
                *      *      *  *
```

---

35.7% identity in 14 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,     183 EEELATLVTTRESMI
UserSeq1,      15 KEITARVKALESML
                *  *      ***
```

---

35.7% identity in 14 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
UserSeq3,      15 KEITARVKALESML
UserSeq1,     183 EEELATLVTTRESMI
                *  *      ***
```

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